

### **INPUT SET: S12085.raw**

**This Raw Listing contains the General Information Section and those Sequences containing ERRORS.**

**Does Not Comply**

2 (1) General Information:

3

4 (i) APPLICANT: Gray, Patrick W.

5

6 (ii) TITLE OF INVENTION: Chitinase Materials and Methods

7

8 (iii) NUMBER OF SEQUENCES: ~~15~~ Please review this response.  
Many more are shown.

9

10 (iv) CORRESPONDENCE ADDRESS:

11 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

12 (B) STREET: 6300 Sears Tower, 233 South Wacker Drive

13 (C) CITY: Chicago

14 (D) STATE: Illinois

15 (E) COUNTRY: United States of America

16 (F) ZIP: 60606-6402

17

18 (v) COMPUTER READABLE FORM:

19 (A) MEDIUM TYPE: Floppy disk

20 (B) COMPUTER: IBM PC compatible

21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

23

24 (vi) CURRENT APPLICATION DATA:

25 (A) APPLICATION NUMBER:

26 (B) FILING DATE:

27 (C) CLASSIFICATION:

28

29 (viii) ATTORNEY/AGENT INFORMATION:

30 (A) NAME: Rin-Laures, Li-Hsien

31 (B) REGISTRATION NUMBER: 33,547

32 (C) REFERENCE/DOCKET NUMBER: 27866/32960

33

34 (ix) TELECOMMUNICATION INFORMATION:

35 (A) TELEPHONE: 312/474-6300

36 (B) TELEFAX: 312/474-0448

37 (C) TELEX: 25-3856

38

39

See attached

## **ERRORED SEQUENCES FOLLOW:**

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/663,618DATE: 08/12/96  
TIME: 14:23:58

INPUT SET: SI2085.raw

40 (2) INFORMATION FOR SEQ ID NO:1:

41

42 (i) SEQUENCE CHARACTERISTICS:

43 (A) LENGTH: 1636 base pairs

44

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: single

46

(D) TOPOLOGY: linear

47

48 (ii) MOLECULE TYPE: cDNA

49

50 (ix) FEATURE:

51 (A) NAME/KEY: CDS

52 (B) LOCATION: 2..1399

53

54 (ix) FEATURE:

55 (A) NAME/KEY: mat\_peptide

56 (B) LOCATION: 65..1399

57

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

59

60 C ATG GTG CGG TCT GTG GCC TGG GCA GGT TTC ATG GTC CTG CTG ATG 46  
Met Val Arg Ser Val Ala Trp Ala Gly Phe Met Val Leu Leu Met  
61 -21 -20 -15 -10

62

63 ATC CCA TGG GGC TCT GCT GCA AAA CTG GTC TGC TAC TTC ACC AAC TGG 94  
Ile Pro Trp Gly Ser Ala Ala Lys Leu Val Cys Tyr Phe Thr Asn Trp  
64 -5 1 5 10

65

66 GCC CAG TAC AGA CAG GGG GAG GCT CGC TTC CTG CCC AAG GAC TTG GAC 142  
Ala Gln Tyr Arg Gln Gly Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp  
67 15 20 25

68

69 CCC AGC CTT TGC ACC CAC CTC ATC TAC GCC TTC GCT GGC ATG ACC AAC 190  
Pro Ser Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn  
70 30 35 40

71

72 CAC CAG CTG AGC ACC ACT GAG TGG AAT GAC GAG ACT CTC TAC CAG GAG 238  
His Gln Leu Ser Thr Thr Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu  
73 45 50 55

74

75 TTC AAT GGC CTG AAG AAG ATG AAT CCC AAG CTG AAG ACC CTG TTA GCC 286  
Phe Asn Gly Leu Lys Met Asn Pro Lys Leu Lys Thr Leu Leu Ala  
76 60 65 70

77

78 ATC GGA GGC TGG AAT TTC GGC ACT CAG AAG TTC ACA GAT ATG GTA GCC 334  
Ile Gly G|GTTT CCCTGCTGAA TGCCTCGCTC 900

79

80 CCTTCAAGAC GAGGGCAGG GAAGGACAGG ACCCTCAGGA ATTCAAGTGCC TTCAACAAACG 960

81

82 TGAGAGAAAG AGAGAAGCCA GCCACAGACC CCTGGGAGCT TCCGCTTTGA AAGAACAGAAG

83

84 ACACGTGGCC TCGTGAGGGG CAAGCTAGGC CCCAGAGGCC CTGGAGGTCT CCAGGGGCCT 1020

85

86 ACACGTGGCC TCGTGAGGGG CAAGCTAGGC CCCAGAGGCC CTGGAGGTCT CCAGGGGCCT 1080

87

88

89

90

91

92

last line reads 1645?ALSO see  
error  
here

46

94

142

190

238

286

334

960

1020

1080

big  
jump  
in  
numbers

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/663,618DATE: 08/12/96  
TIME: 14:24:04

INPUT SET: SI2085.raw

|     |   |      |
|-----|---|------|
| 93  | GCAGAAGGAA AGAAGGGGGC CCTGCTACCT GTTCTTGGGC CTCAGGCTCT GCACAGACAA   | 1140 |
| 94  |   |      |
| 95  | GCAGCCCTTG CTTTCGGAGC TCCTGTCCAA AGTAGGGATG CGGATCCTGC TGGGGCCGCC   | 1200 |
| 96  |   |      |
| 97  | ACGGCCTGGT GGTGGGAAGG CCGGCAGCGG GCGGAGGGGA TCCAGCCACT TCCCCCTCTT   | 1260 |
| 98  |   |      |
| 99  | CTTCTGAAGA TCAGAACATT CAGCTCTGGA GAACAGTGGT TGCCTGGGG CTTTTGCCAC    | 1320 |
| 100 |   |      |
| 101 | TCCTTGTCCC CCGTGATCTC CCCTCACACT TTGCCATTTG CTTGTACTGG GACATTGTTTC  | 1380 |
| 102 |   |      |
| 103 | TTTCCGGCCG AGGTGCCACC ACCCTGCCCC CACTAAGAGA CACATACAGA GTGGGCCCG    | 1440 |
| 104 |   |      |
| 105 | GGCTGGAGAA AGAGCTGCCT GGATGAGAAA CAGCTCAGCC AGTGGGGATG AGGTCACCAG   | 1500 |
| 106 |   |      |
| 107 | GGGAGGGAGCC TGTGCGTCCC AGCTGAAGGC AGTGGCAGGG GAGCAGGTTTC CCCAAGGGCC | 1560 |
| 108 |   |      |
| 109 | CTGGCACCCC CACAAGCTGT CCCTGCAGGG CCATCTGACT GCCAAGCCAG ATTCTCTTGA   | 1620 |
| 110 |   |      |
| 111 | ATAAAGTATT CTAGTGTGGA AACGC   | 1645 |
| 112 |   |      |

257 (2) INFORMATION FOR SEQ ID NO:8:

258

--&gt; 259 (i) SEQUENCE CHARACTERISTICS:

- 260 (A) LENGTH: 170 base pairs
- 261 (B) TYPE: nucleic acid
- 262 (C) STRANDEDNESS: single
- 263 (D) TOPOLOGY: unknown

only 169 shown,

See more detail  
in attached pages

264

265

266

267

268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

269

270

271

272

273

274

275

276

277

278

279

280

281

282

283

284

285

286

287

288

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Val | Met | Arg | Leu | Phe | Pro | Cys | Phe | Leu | Gln | Leu | Leu | Ala | Gly |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Ala | Leu | Pro | Ala | Val | Pro | Pro | Gln | Gln | Trp | Ala | Leu | Ser | Ala | Gly |
|     |     |     |     |     | 20  |     |     |     |     | 25  |     |     | 30  |     |     |
| Asn | Gly | Ser | Ser | Glu | Val | Glu | Val | Val | Pro | Phe | Gln | Glu | Val | Trp | Gly |
|     |     |     |     |     | 35  |     |     |     |     | 40  |     |     | 45  |     |     |
| Arg | Ser | Tyr | Cys | Arg | Ala | Leu | Glu | Arg | Leu | Val | Asp | Val | Val | Ser | Glu |
|     |     |     |     |     | 50  |     |     |     |     | 55  |     |     | 60  |     |     |
| Tyr | Pro | Ser | Glu | Val | Glu | His | Met | Phe | Ser | Pro | Ser | Cys | Val | Ser | Leu |
|     |     |     |     |     | 65  |     |     |     |     | 70  |     |     | 75  |     | 80  |
| Leu | Arg | Cys | Thr | Gly | Cys | Cys | Gly | Asp | Glu | Asn | Leu | His | Cys | Val | Pro |
|     |     |     |     |     | 85  |     |     |     |     | 90  |     |     | 95  |     |     |
| Val | Glu | Thr | Ala | Asn | Val | Thr | Met | Gln | Leu | Leu | Lys | Ile | Arg | Ser | Gly |
|     |     |     |     |     | 100 |     |     |     |     | 105 |     |     | 110 |     |     |

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/663,618DATE: 08/12/96  
TIME: 14:24:09

INPUT SET: S12085.raw

289  
290 Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys  
291 115 120 125  
292  
293 Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro  
294 130 135 140  
295  
296 Lys Gly Arg Gly Lys Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys  
297 145 150 155  
298  
299 His Leu Cys Gly Asp Ala Val Pro Arg Arg ← 169  
300 160 165  
301 (i) SEQUENCE CHARACTERISTICS:  
302 (A) LENGTH: 12 amino acids  
303 (B) TYPE: amino acid  
304 (C) STRANDEDNESS: single  
305 (D) TOPOLOGY: linear  
306  
307 (ii) MOLECULE TYPE: peptide  
308  
--> 309 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:  
310  
311 Trp Arg Lys Phe Ala Leu Leu Gly Ser Gly Pro Thr  
312 1 5 10  
313  
314

--> 315 (2) INFORMATION FOR SEQ ID NO:159:

316  
317 (i) SEQUENCE CHARACTERISTICS:  
318 (A) LENGTH: 12 amino acids  
319 (B) TYPE: amino acid  
320 (C) STRANDEDNESS: single  
321 (D) TOPOLOGY: linear  
322  
323 (ii) MOLECULE TYPE: peptide  
324  
325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:  
326  
327 His Arg Ala Tyr Arg Ile Ala Thr Met Phe Ser Gly  
328 1 5 10  
329  
330

See  
next  
page

363 (2) INFORMATION FOR SEQ ID NO:162:

364  
365 (i) SEQUENCE CHARACTERISTICS:  
366 (A) LENGTH: 12 amino acids  
367 (B) TYPE: amino acid  
368 (C) STRANDEDNESS: single  
369 (D) TOPOLOGY: linear  
370  
371 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly  
1 5 10 15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly  
20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly  
35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu  
50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu  
65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro  
85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly  
100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys  
115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro  
130 135 140

Lys Gly Arg Gly Lys Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys  
145 150 155

His Leu Cys Gly Asp Ala Val Pro Arg Arg  
160 165

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

main heading missing.  
Also, this jumps from  
Seq-8 to 158?

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Trp Arg Lys Phe Ala Leu Leu Gly Ser Gly Pro Thr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

His Arg Ala Tyr Arg Ile Ala Thr Met Phe Ser Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Arg Gly Leu Met Arg Arg Ser Thr Lys Thr Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Ala Arg His Arg Met Phe Gln Trp Ala Met Val Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ile Met Ile Gly Lys Glu Gly Ala Val Ser Ser Ser  
1                   5                           10

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: 73 2 0.5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp Gln Asn Arg Thr His Lys Val Val Ser Gly Arg  
1                   5                   10

Now it  
is back to  
seq 24 ??  
& continues  
on to seq 70  
sel

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: 78 2 1.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala Arg Lys His Lys Val Thr  
1               5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: 40 3 1.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Gln Val Thr Arg Leu His Lys Val Ile His  
1               5                   10